MC010PI

SEQUENCE LISTING

<110> Merck & Co., Inc.
University of British Columbia

<120> APOPTOSIS MODULATORS THAT INTERACT WITH
THE HUNTINGTON'S DISEASE GENE

<130> MC010PI

<140> 09/701,205
<141> 2000-11-27

<150> PCT/US99/11743
<151> 1999-05-27

<150> 09/085,199
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<160> 43

<170> FastSEQ for Windows Version 4.0

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<212> DNA
<213> Human

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<223> n = A,T,C or G

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gtggtggtga tccctgcaga ggcctcatcc cccgacagcg agccagtcct agagaaggat   240
gacctcatgg acatggatgc ctctcagcag aatttatttg acaacaagtt tgatgacntc   300
tttggcagtt catccagcag tgatcccttc aatttcaaca gtcaaaatgg tgtgaacaag   360
gatgagaagg accacttaat tgagcgacta tacagagaga tcagtggatt gaaggcacag   420
ctagaaaaca tgaagactga gagccagcgg gttgtgctgc agctgaaggg ccacgtcagc   480
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aaagagctgg aggattcgtt ggagcgcatc agtgaccagg gccagcggga gactcaagaa   840
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ttatctgctc ttcggaaaga actgcaggac actcagctca aactggccag cacagaggaa   1080
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<211> 386
<212> PRT
<213> Human

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Lys Arg Val Ile Gln Ile Pro Gln Leu Pro Glu Asn Pro Pro Asn Phe
            35                  40                  45
Leu Arg Ala Ser Ala Leu Ser Glu His Ile Ser Pro Val Val Val Ile
    50                  55                  60
Pro Ala Glu Ala Ser Ser Pro Asp Ser Glu Pro Val Leu Glu Lys Asp
65                  70                  75                      80
Asp Leu Met Asp Met Asp Ala Ser Gln Gln Asn Leu Phe Asp Asn Lys
                85                  90                  95
Phe Asp Asp Phe Gly Ser Ser Ser Ser Ser Asp Pro Phe Asn Phe Asn
            100                 105                 110
Ser Gln Asn Gly Val Asn Lys Asp Glu Lys Asp His Leu Ile Glu Arg
    115                 120                 125
Leu Tyr Arg Glu Ile Ser Gly Leu Lys Ala Gln Leu Glu Asn Met Lys
    130                 135                 140
Thr Glu Ser Gln Arg Val Val Leu Gln Leu Lys Gly His Val Ser Glu
145                 150                 155                 160
Leu Glu Ala Asp Leu Ala Glu Gln Gln His Leu Arg Gln Gln Ala Ala
                165                 170                 175
Asp Asp Cys Glu Phe Leu Arg Ala Glu Leu Asp Glu Leu Arg Gln Arg
            180                 185                 190
Glu Asp Thr Glu Lys Ala Gln Arg Ser Leu Ser Glu Ile Glu Arg Lys
            195                 200                 205
Ala Gln Ala Asn Glu Gln Arg Tyr Ser Lys Leu Lys Glu Lys Tyr Ser
    210                 215                 220
Glu Leu Val Gln Asn His Ala Asp Leu Leu Arg Lys Asn Ala Glu Val
225                 230                 235                 240
Thr Lys Gln Val Ser Met Ala Arg Gln Ala Gln Val Asp Leu Glu Arg
            245                 250                 255
Glu Lys Lys Glu Leu Glu Asp Ser Leu Glu Arg Ile Ser Asp Gln Gly
            260                 265                 270
Gln Arg Lys Thr Gln Glu Gln Leu Glu Val Leu Glu Ser Leu Lys Gln
            275                 280                 285
Glu Leu Gly Thr Ser Gln Arg Glu Leu Gln Val Leu Gln Gly Ser Leu
    290                 295                 300
Glu Thr Ser Ala Gln Ser Glu Ala Asn Trp Ala Ala Glu Phe Ala Glu
305                 310                 315                 320
Leu Glu Lys Glu Arg Asp Ser Leu Val Ser Gly Ala Ala His Arg Glu
            325                 330                 335
Glu Glu Leu Ser Ala Leu Arg Lys Glu Leu Gln Asp Thr Gln Leu Lys
            340                 345                 350
Leu Ala Ser Thr Glu Glu Ser Met Cys Gln Leu Ala Lys Asp Gln Arg
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Asp Ala
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<210> 3
<211> 4796
<212> DNA
<213> Human

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tacagcgagc tggttcagaa ccacgctgac ctgctgcgga agaatgcaga ggtgaccaaa  1440
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- 3 -

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<211> 914
<212> PRT
<213> Human

<400> 4

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Asn Pro Arg Phe Pro Gly Asn Leu Gln Met Ser Asp Arg Gln Leu Asp
        35                  40                  45
Glu Ala Gly Glu Ser Asp Val Asn Asn Phe Phe Gln Leu Thr Val Glu
    50                  55                  60
Met Phe Asp Tyr Leu Glu Cys Glu Leu Asn Leu Phe Gln Thr Val Phe
65                  70                  75                  80
Asn Ser Leu Asp Met Ser Arg Ser Val Ser Val Thr Ala Ala Gly Gln
                85                  90                  95
Cys Arg Leu Ala Pro Leu Ile Gln Val Ile Leu Asp Cys Ser His Leu
            100                 105                 110
Tyr Asp Tyr Thr Val Lys Leu Leu Phe Lys Leu His Ser Cys Leu Pro
        115                 120                 125
Ala Asp Thr Leu Gln Gly His Arg Asp Arg Phe Met Glu Gln Phe Thr
        130                 135                 140
Lys Leu Lys Asp Leu Phe Tyr Arg Ser Ser Asn Leu Gln Tyr Phe Lys
145                 150                 155                 160
Arg Leu Ile Gln Ile Pro Gln Leu Pro Glu Asn Pro Pro Asn Phe Leu
                165                 170                 175
Arg Ala Ser Ala Leu Ser Glu His Ile Ser Pro Val Val Val Ile Pro
            180                 185                 190
Ala Glu Ala Ser Ser Pro Asp Ser Glu Pro Val Leu Glu Lys Asp Asp
        195                 200                 205
Leu Met Asp Met Asp Ala Ser Gln Gln Asn Leu Phe Asp Asn Lys Phe
    210                 215                 220
Asp Asp Ile Phe Gly Ser Ser Phe Ser Ser Asp Pro Phe Asn Phe Asn
225                 230                 235                 240
Ser Gln Asn Gly Val Asn Lys Asp Glu Lys Asp His Leu Ile Glu Arg
                245                 250                 255
Leu Tyr Arg Glu Ile Ser Gly Leu Lys Ala Gln Leu Glu Asn Met Lys
            260                 265                 270
Thr Glu Ser Gln Arg Val Val Leu Gln Leu Lys Gly His Val Ser Glu
            275                 280                 285
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-4-

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Leu Glu Ala Asp Leu Ala Glu Gln Gln His Leu Arg Gln Gln Ala Ala
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Asp Asp Cys Glu Phe Leu Arg Ala Glu Leu Asp Glu Leu Arg Arg Gln
305                 310                 315                 320
Arg Glu Asp Thr Glu Lys Ala Gln Arg Ser Leu Ser Glu Ile Glu Arg
                325                 330                 335
Lys Ala Gln Ala Asn Glu Gln Arg Tyr Ser Lys Leu Lys Glu Lys Tyr
                340                 345                 350
Ser Glu Leu Val Gln Asn His Ala Asp Leu Leu Arg Lys Asn Ala Glu
        355                 360                 365
Val Thr Lys Gln Val Ser Met Ala Arg Gln Ala Gln Val Asp Leu Glu
370                 375                 380
Arg Glu Lys Lys Glu Leu Glu Asp Ser Leu Glu Arg Ile Ser Asp Gln
385                 390                 395                 400
Gly Gln Arg Lys Thr Gln Glu Gln Leu Glu Val Leu Glu Ser Leu Lys
                405                 410                 415
Gln Glu Leu Gly Thr Ser Gln Arg Glu Leu Gln Val Leu Gln Gly Ser
                420                 425                 430
Leu Glu Thr Ser Ala Gln Ser Glu Ala Asn Trp Ala Ala Glu Phe Ala
        435                 440                 445
Glu Leu Glu Lys Glu Arg Asp Ser Leu Val Ser Gly Ala Ala His Arg
    450                 455                 460
Glu Glu Glu Leu Ser Ala Leu Arg Lys Glu Leu Gln Asp Thr Gln Leu
465                 470                 475                 480
Lys Leu Ala Ser Thr Glu Glu Ser Met Cys Gln Leu Ala Lys Asp Gln
                485                 490                 495
Arg Lys Met Leu Leu Val Gly Ser Arg Lys Ala Ala Glu Gln Val Ile
                500                 505                 510
Gln Asp Ala Leu Asn Gln Leu Glu Glu Pro Pro Leu Ile Ser Cys Ala
        515                 520                 525
Gly Ser Ala Asp His Leu Leu Ser Thr Val Thr Ser Ile Ser Ser Cys
    530                 535                 540
Ile Glu Gln Leu Glu Lys Ser Trp Ser Gln Tyr Leu Ala Cys Pro Glu
545                 550                 555                 560
Asp Ile Ser Gly Leu Leu His Ser Ile Thr Leu Leu Ala His Leu Thr
                565                 570                 575
Ser Asp Ala Ile Ala His Gly Ala Thr Thr Cys Leu Arg Ala Pro Pro
            580                 585                 590
Glu Pro Ala Asp Ser Leu Thr Glu Ala Cys Lys Gln Tyr Gly Arg Glu
    595                 600                 605
Thr Leu Ala Tyr Leu Ala Ser Leu Glu Glu Glu Gly Ser Leu Glu Asn
    610                 615                 620
Ala Asp Ser Thr Ala Met Arg Asn Cys Leu Ser Lys Ile Lys Ala Ile
625                 630                 635                 640
Gly Glu Glu Leu Leu Pro Arg Gly Leu Asp Ile Lys Gln Glu Glu Leu
                645                 650                 655
Gly Asp Leu Val Asp Lys Glu Met Ala Ala Thr Ser Ala Ala Ile Glu
            660                 665                 670
Thr Cys Thr Ala Arg Ile Glu Glu Met Leu Ser Lys Ser Arg Ala Gly
    675                 680                 685
Asp Thr Gly Val Lys Leu Glu Val Asn Glu Arg Ile Leu Arg Cys Cys
    690                 695                 700
Thr Ser Leu Met Gln Ala Ile Gln Val Leu Ile Val Ala Ser Lys Asp
705                 710                 715                 720
Leu Gln Arg Glu Ile Val Glu Ser Gly Arg Gly Thr Ala Ser Pro Lys
                725                 730                 735
Glu Phe Tyr Ala Lys Asn Ser Arg Trp Thr Glu Gly Leu Ile Ser Ala
            740                 745                 750
Ser Lys Ala Val Gly Trp Gly Ala Thr Val Met Val Asp Ala Ala Asp
        755                 760                 765
Leu Val Val Gln Gly Arg Gly Lys Phe Glu Glu Leu Met Val Cys Ser
    770                 775                 780
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His Glu Ile Ala Ala Ser Thr Ala Gln Leu Val Ala Ala Ser Lys Val
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Lys Ala Asp Lys Asp Ser Pro Asn Leu Ala Gln Leu Gln Gln Ala Ser
                805                 810                 815
Arg Gly Val Asn Gln Ala Thr Ala Gly Val Val Ala Ser Thr Ile Ser
            820                 825                 830
Gly Lys Ser Gln Ile Glu Glu Thr Asp Asn Met Asp Phe Ser Ser Met
        835                 840                 845
Thr Leu Thr Gln Ile Lys Arg Gln Glu Met Asp Ser Gln Val Arg Val
    850                 855                 860
Leu Glu Leu Glu Asn Glu Leu Gln Lys Glu Arg Gln Lys Leu Gly Glu
865                 870                 875                 880
Leu Arg Lys Lys His Tyr Glu Leu Ala Gly Val Ala Glu Gly Trp Glu
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Glu Gly Thr Glu Ala Ser Pro Pro Thr Leu Gln Glu Val Val Thr Glu
        900                 905                 910
Lys Glu
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<210> 5
<211> 1090
<212> PRT
<213> Human

<400> 5
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            20                  25                  30
Ala Gly Ser Trp Glu Arg Cys Pro Pro Leu Pro Pro Ala Gly Arg Leu
        35                  40                  45
Gln Gly Thr Asp His Pro Trp Gly Trp Gly Arg Leu Ala Gly Gly Gly
    50                  55                  60
Glu Arg Gly Gly Leu Trp Glu Gly Leu Ser His Ser Gln Arg Leu Ile
65                  70                  75                  80
His Leu Ile Leu Leu Ser Leu Pro Leu Leu Val Phe Gln Thr Val Ser
            85                  90                  95
Ile Asn Lys Ala Ile Asn Thr Gln Glu Val Ala Val Lys Glu Lys His
            100                 105                 110
Ala Arg Thr Cys Ile Leu Gly Thr His His Glu Lys Gly Ala Gln Thr
        115                 120                 125
Phe Trp Ser Val Val Asn Arg Leu Pro Leu Ser Ser Asn Ala Val Leu
    130                 135                 140
Cys Trp Lys Phe Cys His Val Phe His Lys Leu Leu Arg Asp Gly His
145                 150                 155                 160
Pro Asn Val Leu Lys Asp Ser Leu Arg Tyr Arg Asn Glu Leu Ser Asp
            165                 170                 175
Met Ser Arg Met Trp Gly His Leu Ser Glu Gly Tyr Gly Gln Leu Cys
        180                 185                 190
Ser Ile Tyr Leu Lys Leu Leu Arg Thr Lys Met Glu Tyr His Thr Lys
    195                 200                 205
Asn Pro Arg Phe Pro Gly Asn Leu Gln Met Ser Asp Arg Gln Leu Asp
    210                 215                 220
Glu Ala Gly Glu Ser Asp Val Asn Asn Phe Phe Gln Leu Thr Val Glu
225                 230                 235                 240
Met Phe Asp Tyr Leu Glu Cys Glu Leu Asn Leu Phe Gln Thr Val Phe
            245                 250                 255
Asn Ser Leu Asp Met Ser Arg Ser Val Ser Val Thr Ala Ala Gly Gln
            260                 265                 270
Cys Arg Leu Ala Pro Leu Ile Gln Val Ile Leu Asp Cys Ser His Leu
        275                 280                 285
Tyr Asp Tyr Thr Val Lys Leu Leu Phe Lys Leu His Ser Cys Leu Pro
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        290                    295                    300
Ala Asp Thr Leu Gln Gly His Arg Asp Arg Phe Met Glu Gln Phe Thr
305                    310                    315                    320
Lys Leu Lys Asp Leu Phe Tyr Arg Ser Ser Asn Leu Gln Tyr Phe Lys
                  325                    330                    335
Arg Leu Ile Gln Ile Pro Gln Leu Pro Glu Asn Pro Pro Asn Phe Leu
             340                    345                    350
Arg Ala Ser Ala Leu Ser Glu His Ile Ser Pro Val Val Val Ile Pro
             355                    360                    365
Ala Glu Ala Ser Ser Pro Asp Ser Glu Pro Val Leu Glu Lys Asp Asp
        370                    375                    380
Leu Met Asp Met Asp Ala Ser Gln Gln Asn Leu Phe Asp Asn Lys Phe
385                    390                    395                    400
Asp Asp Ile Phe Gly Ser Ser Phe Ser Ser Asp Pro Phe Asn Phe Asn
                  405                    410                    415
Ser Gln Asn Gly Val Asn Lys Asp Glu Lys Asp His Leu Ile Glu Arg
             420                    425                    430
Leu Tyr Arg Glu Ile Ser Gly Leu Lys Ala Gln Leu Glu Asn Met Lys
        435                    440                    445
Thr Glu Ser Gln Arg Val Val Leu Gln Leu Lys Gly His Val Ser Glu
     450                    455                    460
Leu Glu Ala Asp Leu Ala Glu Gln Gln His Leu Arg Gln Gln Ala Ala
465                    470                    475                    480
Asp Asp Cys Glu Phe Leu Arg Ala Glu Leu Asp Glu Leu Arg Arg Gln
                  485                    490                    495
Arg Glu Asp Thr Glu Lys Ala Gln Arg Ser Leu Ser Glu Ile Glu Arg
             500                    505                    510
Lys Ala Gln Ala Asn Glu Gln Arg Tyr Ser Lys Leu Lys Glu Lys Tyr
        515                    520                    525
Ser Glu Leu Val Gln Asn His Ala Asp Leu Leu Arg Lys Asn Ala Glu
     530                    535                    540
Val Thr Lys Gln Val Ser Met Ala Arg Gln Ala Gln Val Asp Leu Glu
545                    550                    555                    560
Arg Glu Lys Lys Glu Leu Glu Asp Ser Leu Glu Arg Ile Ser Asp Gln
                  565                    570                    575
Gly Gln Arg Lys Thr Gln Glu Gln Leu Glu Val Leu Glu Ser Leu Lys
             580                    585                    590
Gln Glu Leu Ala Thr Ser Gln Arg Glu Leu Gln Val Leu Gln Gly Ser
        595                    600                    605
Leu Glu Thr Ser Ala Gln Ser Glu Ala Asn Trp Ala Ala Glu Phe Ala
        610                    615                    620
Glu Leu Glu Lys Glu Arg Asp Ser Leu Val Ser Gly Ala Ala His Arg
625                    630                    635                    640
Glu Glu Glu Leu Ser Ala Leu Arg Lys Glu Leu Gln Asp Thr Gln Leu
                  645                    650                    655
Lys Leu Ala Ser Thr Glu Glu Ser Met Cys Gln Leu Ala Lys Asp Gln
                  660                    665                    670
Arg Lys Met Leu Leu Val Gly Ser Arg Lys Ala Ala Glu Gln Val Ile
        675                    680                    685
Gln Asp Ala Leu Asn Gln Leu Glu Glu Pro Pro Leu Ile Ser Cys Ala
        690                    695                    700
Gly Ser Ala Asp His Leu Leu Ser Thr Val Thr Ser Ile Ser Ser Cys
705                    710                    715                    720
Ile Glu Gln Leu Glu Lys Ser Trp Ser Gln Tyr Leu Ala Cys Pro Glu
                  725                    730                    735
Asp Ile Ser Gly Leu Leu His Ser Ile Thr Leu Leu Ala His Leu Thr
             740                    745                    750
Ser Asp Ala Ile Ala His Gly Ala Thr Thr Cys Leu Arg Ala Pro Pro
        755                    760                    765
Glu Pro Ala Asp Ser Leu Thr Glu Ala Cys Lys Gln Tyr Gly Arg Glu
        770                    775                    780
Thr Leu Ala Tyr Leu Ala Ser Leu Glu Glu Glu Gly Ser Leu Glu Asn
```

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785                      790                      795                      800
Ala Asp Ser Thr Ala Met Arg Asn Cys Leu Ser Lys Ile Lys Ala Ile
                805                      810                      815
Gly Glu Glu Leu Leu Pro Arg Gly Leu Asp Ile Lys Gln Glu Glu Leu
            820                      825                      830
Gly Asp Leu Val Asp Lys Glu Met Ala Ala Thr Ser Ala Ala Ile Glu
            835                      840                      845
Thr Ala Thr Ala Arg Ile Glu Glu Met Leu Ser Lys Ser Arg Ala Gly
        850                      855                      860
Asp Thr Gly Val Lys Leu Glu Val Asn Glu Arg Ile Leu Gly Cys Cys
865                      870                      875                      880
Thr Ser Leu Met Gln Ala Ile Gln Val Leu Ile Val Ala Ser Lys Asp
                885                      890                      895
Leu Gln Arg Glu Ile Val Glu Ser Gly Arg Gly Thr Ala Ser Pro Lys
            900                      905                      910
Glu Phe Tyr Ala Lys Asn Ser Arg Trp Thr Glu Gly Leu Ile Ser Ala
        915                      920                      925
Ser Lys Ala Val Gly Trp Gly Ala Thr Val Met Val Asp Ala Ala Asp
        930                      935                      940
Leu Val Val Gln Gly Arg Gly Lys Phe Glu Glu Leu Met Val Cys Ser
945                      950                      955                      960
His Glu Ile Ala Ala Ser Thr Ala Gln Leu Val Ala Ala Ser Lys Val
                965                      970                      975
Lys Ala Asp Lys Asp Ser Pro Asn Leu Ala Gln Leu Gln Gln Ala Ser
            980                      985                      990
Arg Gly Val Asn Gln Ala Thr Ala Gly Val Val Ala Ser Thr Ile Ser
        995                      1000                     1005
Gly Lys Ser Gln Ile Glu Glu Thr Asp Asn Met Asp Phe Ser Ser Met
    1010                     1015                     1020
Thr Leu Thr Gln Ile Lys Arg Gln Glu Met Asp Ser Gln Val Arg Val
1025                     1030                     1035                     1040
Leu Glu Leu Glu Asn Glu Leu Gln Lys Glu Arg Gln Lys Leu Gly Glu
                1045                     1050                     1055
Leu Arg Lys Lys His Tyr Glu Leu Ala Gly Val Ala Glu Gly Trp Glu
                1060                     1065                     1070
Glu Gly Thr Glu Ala Ser Pro Pro Thr Leu Gln Glu Val Val Thr Glu
            1075                     1080                     1085
Lys Glu
    1090

<210> 6
<211> 3251
<212> DNA
<213> Human

<400> 6
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ccgccacgag ctggcccagc tgagggctgc ccagctggag cgcgagcgga gccagggcct       120
gcgtgaggag gctgagagga aggccagtgc cacggaggcg cgctacaaca agctgaagga       180
aaagcacagt gagctcgtcc atgtgcacgc ggagctgctc agaaagaacg cggacacagc       240
caagcagctg acggtgacgc agcaaagcca ggaggaggtg cgcgcgggtga aggagcagct       300
ggccttccag gtggagcagg tgaagcggga gtcggagttg aagctagagg agaagagcga       360
ccagcaggag aagctcaaga gggagctgga ggccaaggcc ggagagctgg cccgcgcgca       420
ggaggccctg agccacacag agcagagcaa gtcggagctg agctcacggc tggacacact       480
gagtgcggag aaggatgctc tgagtggagc tgtgcggcag cgggaggcag acctgctggc       540
ggcgcagagc ctggtgcgcg agacagaggc ggcgctgagc cgggagcagc agcgcagctc       600
ccaggagcag ggcgagttgc aggggccggct ggcagagagg gagtctcagg agcaggggct       660
gcggcagagg ctgctggacg agcagttcgc agtgttgcgg ggcgctgctg ccgaggccgc       720
gggcatcctg caggatgccg tgagcaagct ggacgacccc ctgcacctgc gctgtaccag       780
ctccccagac tacctggtga gcagggccca ggaggccttg gatgccgtga gcaccctgga       840
ggagggccac gcccagtacc tgacctcctt ggcagacgcc tccgccctgg tggcagctct       900
gacccgcttc tcccacctgg ctgcggatac catcatcaat ggcggtgcca cctcgcacct       960
```

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ggctcccacc gaccctgccg accgcctcat agacacctgc agggagtgcg gggcccgggc    1020
tctggagctc atggggcagc tgcaggacca gcaggctctg cggcacatgc aggccagcct    1080
ggtgcggaca cccctgcagg gcatccttca gctgggccaa gaactgaaac ccaagagcct    1140
agatgtgcgg caggaggagc tggggggccgt ggtcgacaag gagatggcgg ccacatccgc    1200
agccattgaa gatgctgtgc ggaggattga ggacatgatg aaccaggcac gccacgccag    1260
ctcggggggtg aagctggagg tgaacgagag gatcctcaac tcctgcacag acctgatgaa    1320
ggctatccgg ctcctggtga cgacatccac tagcctgcag aaggagatcg tggagagcgg    1380
caggggggca gccacgcagc aggaatttta cgccaagaac tcgcgctgga ccgaaggcct    1440
catctcggcc tccaaggctg tgggctgggg agccacacag ctggtggagg cagctgacaa    1500
ggtggtgctt cacacgggca agtatgagga gctcatcgtc tgctcccacg agatcgcagc    1560
cagcacggcc cagctggtgg cggcctccaa ggtgaaggcc aacaagcaca gcccccacct    1620
gagccgcctg caggaatgtt ctcgcacagt caatgagagg gctgccaatg tggtggcctc    1680
caccaagtca ggccaggagc agattgagga cagagacacc atggatttct ccggcctgtc    1740
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gacgctggag gctgaacgca tgcggctggg ggagttgcgg aagcaacact acgtgctggc    1860
tggggcatca ggcagccctg gagaggaggt ggccatccgg cccagcactg cccccccgaag    1920
tgtaaccacc aagaaaccac ccctggccca gaagcccagc gtggcccccca gacaggacca    1980
ccagcttgac aaaaaggatg gcatctaccc agctcaactc gtgaactact aggcccccca    2040
ggggtccagc agggtggctg gtgacaggcc tgggcctctg caactgccct gacaggaccg    2100
agaggccttg cccctccacc tggtgcccaa gcctccccgcc ccaccgtctg gatcaatgtc    2160
ctcaaggccc ctggccctta ctgagcctgc agggtcctgc gccatgtggg tggtgcttct    2220
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gggccagcgt ggggctccct gccttctgga ctcctgaagg tcgtgatgg atggaaggca    2460
cacagcccgt gccggctgat gggacgaggg tcaggcatcc tgtctgtggc cttctggggc    2520
accgattcta ccaggccctc cagctgcgtg gtctccgcag accaggctct gtgtgggcta    2580
gaggaatgtc gcccattacc tcctcaggcc ctggccctcg ggcctccgtg atgggagccc    2640
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gcccaggccc tgccttcact cctggagttt ccatttccag ctggaatctg cagccacccc    2760
catttcctgt tttccattcc cccgttctgg ccgcgcccca ctgcccacct gaaggggtgg    2820
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cagaaaccca ggtgctggac cagggccctc agggagggac cctgcggcta gagtgggcta    2940
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gcaggagggg tgggaccagg ctgggaggac agagccagca gctgccatgc cctcctgctc    3060
cccccacccc agccctagcc ctttagcctt tcaccctgtg ctctgtgaaag gctaccaaat    3120
actggccaag gtcaggagga gcaaaaatga gccagcacca gcgccttggc tttgtgttag    3180
catttcctcc tgaagtgttc tgttggcaat aaaatgcact ttgactgtta aaaaaaaaaa    3240
aaaaaaaaaa a                                                          3251
```

<210> 7
<211> 676
<212> PRT
<213> Human

<400> 7
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Gly Glu Leu Glu Glu Gln Arg Lys Gln Lys Gln Lys Ala Leu Val Asp
1               5                   10                  15
Asn Glu Gln Leu Arg His Glu Leu Ala Gln Leu Arg Ala Ala Gln Leu
            20                  25                  30
Glu Arg Glu Arg Ser Gln Gly Leu Arg Glu Glu Ala Glu Arg Lys Ala
        35                  40                  45
Ser Ala Thr Glu Ala Arg Tyr Asn Lys Leu Lys Glu Lys His Ser Glu
    50                  55                  60
Leu Val His Val His Ala Glu Leu Leu Arg Lys Asn Ala Asp Thr Ala
65                  70                  75                  80
Lys Gln Leu Thr Val Thr Gln Gln Ser Gln Glu Glu Val Ala Arg Val
            85                  90                  95
Lys Glu Gln Leu Ala Phe Gln Val Glu Gln Val Lys Arg Glu Ser Glu
            100                 105                 110
Leu Lys Leu Glu Glu Lys Ser Asp Gln Gln Glu Lys Leu Lys Arg Glu
        115                 120                 125
```

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```
Leu Glu Ala Lys Ala Gly Glu Leu Ala Arg Ala Gln Glu Ala Leu Ser
    130                     135                 140
His Thr Glu Gln Ser Lys Ser Glu Leu Ser Ser Arg Leu Asp Thr Leu
145                 150                 155                     160
Ser Ala Glu Lys Asp Ala Leu Ser Gly Ala Val Arg Gln Arg Glu Ala
                165                 170                 175
Asp Leu Leu Ala Ala Gln Ser Leu Val Arg Glu Thr Glu Ala Ala Leu
                180                 185                 190
Ser Arg Glu Gln Gln Arg Ser Ser Gln Glu Gln Gly Glu Leu Gln Gly
            195                 200                 205
Arg Leu Ala Glu Arg Glu Ser Gln Glu Gln Gly Leu Arg Gln Arg Leu
    210                 215                 220
Leu Asp Glu Gln Phe Ala Val Leu Arg Gly Ala Ala Ala Glu Ala Ala
225                 230                 235                     240
Gly Ile Leu Gln Asp Ala Val Ser Lys Leu Asp Asp Pro Leu His Leu
                245                 250                 255
Arg Cys Thr Ser Ser Pro Asp Tyr Leu Val Ser Arg Ala Gln Glu Ala
                260                 265                 270
Leu Asp Ala Val Ser Thr Leu Glu Glu Gly His Ala Gln Tyr Leu Thr
            275                 280                 285
Ser Leu Ala Asp Ala Ser Ala Leu Val Ala Ala Leu Thr Arg Phe Ser
    290                 295                 300
His Leu Ala Ala Asp Thr Ile Ile Asn Gly Gly Ala Thr Ser His Leu
305                 310                 315                     320
Ala Pro Thr Asp Pro Ala Asp Arg Leu Ile Asp Thr Cys Arg Glu Cys
                325                 330                 335
Gly Ala Arg Ala Leu Glu Leu Met Gly Gln Leu Gln Asp Gln Gln Ala
            340                 345                 350
Leu Arg His Met Gln Ala Ser Leu Val Arg Thr Pro Leu Gln Gly Ile
    355                 360                 365
Leu Gln Leu Gly Gln Glu Leu Lys Pro Lys Ser Leu Asp Val Arg Gln
    370                 375                 380
Glu Glu Leu Gly Ala Val Val Asp Lys Glu Met Ala Ala Thr Ser Ala
385                 390                 395                     400
Ala Ile Glu Asp Ala Val Arg Arg Ile Glu Asp Met Met Asn Gln Ala
                405                 410                 415
Arg His Ala Ser Ser Gly Val Lys Leu Glu Val Asn Glu Arg Ile Leu
            420                 425                 430
Asn Ser Cys Thr Asp Leu Met Lys Ala Ile Arg Leu Leu Val Thr Thr
        435                 440                 445
Ser Thr Ser Leu Gln Lys Glu Ile Val Glu Ser Gly Arg Gly Ala Ala
    450                 455                 460
Thr Gln Gln Glu Phe Tyr Ala Lys Asn Ser Arg Trp Thr Glu Gly Leu
465                 470                 475                     480
Ile Ser Ala Ser Lys Ala Val Gly Trp Gly Ala Thr Gln Leu Val Glu
                485                 490                 495
Ala Ala Asp Lys Val Val Leu His Thr Gly Lys Tyr Glu Glu Leu Ile
            500                 505                 510
Val Cys Ser His Glu Ile Ala Ala Ser Thr Ala Gln Leu Val Ala Ala
    515                 520                 525
Ser Lys Val Lys Ala Asn Lys His Ser Pro His Leu Ser Arg Leu Gln
    530                 535                 540
Glu Cys Ser Arg Thr Val Asn Glu Arg Ala Ala Asn Val Val Ala Ser
545                 550                 555                     560
Thr Lys Ser Gly Gln Glu Gln Ile Glu Asp Arg Asp Thr Met Asp Phe
                565                 570                 575
Ser Gly Leu Ser Leu Ile Lys Leu Lys Lys Gln Glu Met Glu Thr Gln
            580                 585                 590
Val Arg Val Leu Glu Leu Glu Lys Thr Leu Glu Ala Glu Arg Met Arg
    595                 600                 605
Leu Gly Glu Leu Arg Lys Gln His Tyr Val Leu Ala Gly Ala Ser Gly
    610                 615                 620
```

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```
Ser Pro Gly Glu Glu Val Ala Ile Arg Pro Ser Thr Ala Pro Arg Ser
625                 630                 635                 640
Val Thr Thr Lys Lys Pro Pro Leu Ala Gln Lys Pro Ser Val Ala Pro
            645                 650                 655
Arg Gln Asp His Gln Leu Asp Lys Lys Asp Gly Ile Tyr Pro Ala Gln
            660                 665                 670
Leu Val Asn Tyr
        675
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```
<210>  8
<211>  2301
<212>  DNA
<213>  Mouse

<400>  8
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ctcggccctg tcagagcaca tcagtcctgt ggtggtgatc ccggcagagg tgtcatcccc   120
agacagtgag cctgtcctgg agaaggatga cctcatggac atggacgcct cccagcagac   180
tttgtttgac aacaagtttg atgacgtctt tggcagctca ttgagcagcg acccttttcaa  240
tttcaacaat caaaatggcg tgaacaagga cgagaaggac cacttgattg aacgcctgta   300
cagagagatc agtggactga cagggcagct ggacaacatg aagattgaga gccagcgggc   360
catgctgcag ctgaagggtc gagtgagtga gctggaggca gagctagcag agcagcagca   420
cttgggccgg caggctatgg atgactgcga gttcctgcgc actgagctgg atgaactgaa   480
gaggcagcga gaggacacgg agaaggcaca gcgcagcctg actgagatag aaagaaaggc   540
ccaggctaat gaacagaggt atagcaagtt aaaagagaag tacagtgaac tggtgcagaa   600
ccatgctgac ctgctgcgga agaacgcaga ggtgaccaaa caggtgtccg tggcccggca   660
agcccaggtg gatttggaaa gagagaaaaa agagctagca gattcctttg cacgtgtaag   720
tgaccaggcc cagcggaaga ctcaagagca acaggatgtt ctagagaacc tgaagcatga   780
actggccacc agcagacagg agctgcaggt cctccacagc aacctggaaa cctctgccca   840
gtcagaagcg aaatggctga cacagatcgc cgagttggag aaggaacaag gcagcttggc   900
gactgttgca gctcagagag aggaagagtt atcagccctc cgagaccagc tggaaagcac   960
ccagatcaag ctggctgggg cccaggaatc catgtgccag caggtgaagg accagaggaa  1020
aaccctcttg gcagggatca ggaaggctgc ggagcgtgag atacaggagg cgctgagcca  1080
gcttgaggaa cccacccTca tcagctgtgc aggatccaca gatcaccttc tctccaaagt  1140
cagctccgtt tccagctgcc tcgagcaact ggaaaagaac ggcagccagt atctggcctg  1200
cccagaagat attagtgagc ttctgcactc gatcacccTg cttgcccact tgaccggtga  1260
cactgtcatc caggggagtg ccaccagcct ccgggcccca ccggagccag ccgactcgtt  1320
gacggaggcc tgtaggcagt atggcagaga aaccctggcc tatctgtcct ccctggagga  1380
agagggaact gtggagaatg ctgacgtcac agcccttagg aattgcctca gcagggtcaa  1440
gacccttggc gaggagctgc tgcccagggg cctggacatc aagcaggaag agctgggtga  1500
cctggtggac aaggagatgg cagccacttc agctgccatt gaagctgcca ccacccggat  1560
agaggaaatt ctcagtaagt cccgagcagg agacacggga gtcaagctgg aggtgaatga  1620
gaggatcctg ggttcctgta ccagcctgat gcaggccatc aaggtgctcg ttgtggcctc  1680
caaggacctc cagaaggaga tagtggagag tggcagggggt agtgcatccc ctaaagaatt  1740
ttacgccaag aactctcggt ggacggaagg gctgatatcc gcctccaaag ctgttggttg  1800
gggagctacc atcatggtgg atgctgctga tcttgtggtc caaggcaaag ggaagttcga  1860
ggagctgatg gtgtgttcac gcgagattgc tgccagtact gcccagctcg tggctgcatc  1920
caaggtgaaa gcgaacaagg gcagcctcaa tctgacccag ctgcagcagg cctctcgagg  1980
agtgaaccag gccacagccg ctgtggtggc ctcaaccatt tctggcaaat ctcagattga  2040
ggaaacagac agtatggact tctcaagcat gacactgacc cagatcaagc gccaggagat  2100
ggattcccag gttagggtgc tggagctgga aaatgacctg cagaaggagc gtcagaaact  2160
aggagagcta cggaagaaac actacgagct ggagggcgtg gctgagggct gggaggaagg  2220
gacagaagca tcaccgtcta ctgtccaaga agcaataccg gacaaagagt agagccaagc  2280
cgacacccca cacatcagaa a                                             2301
```

```
<210>  9
<211>  756
<212>  PRT
<213>  Mouse

<400>  9
Ala Arg Gly Leu Ile Gln Ile Pro Gln Leu Pro Glu Asn Pro Pro Asn
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 1                   5                   10                  15
Phe Leu Arg Ala Ser Ala Leu Ser Glu His Ile Ser Pro Val Val Val
            20                  25                  30
Ile Pro Ala Glu Val Ser Ser Pro Asp Ser Glu Pro Val Leu Glu Lys
            35                  40                  45
Asp Asp Leu Met Asp Met Asp Ala Ser Gln Gln Thr Leu Phe Asp Asn
            50                  55                  60
Lys Phe Asp Asp Val Phe Gly Ser Ser Leu Ser Ser Asp Pro Phe Asn
65                  70                  75                  80
Phe Asn Asn Gln Asn Gly Val Asn Lys Asp Glu Lys Asp His Leu Ile
                85                  90                  95
Glu Arg Leu Tyr Arg Glu Ile Ser Gly Leu Thr Gly Gln Leu Asp Asn
            100                 105                 110
Met Lys Ile Glu Ser Gln Arg Ala Met Leu Gln Leu Lys Gly Arg Val
            115                 120                 125
Ser Glu Leu Glu Ala Glu Leu Ala Glu Gln Gln His Leu Gly Arg Gln
            130                 135                 140
Ala Met Asp Asp Cys Glu Phe Leu Arg Thr Glu Leu Asp Glu Leu Lys
145                 150                 155                 160
Arg Gln Arg Glu Asp Thr Glu Lys Ala Gln Arg Ser Leu Thr Glu Ile
                165                 170                 175
Glu Arg Lys Ala Gln Ala Asn Glu Gln Arg Tyr Ser Lys Leu Lys Glu
            180                 185                 190
Lys Tyr Ser Glu Leu Val Gln Asn His Ala Asp Leu Leu Arg Lys Asn
            195                 200                 205
Ala Glu Val Thr Lys Gln Val Ser Val Ala Arg Gln Ala Gln Val Asp
            210                 215                 220
Leu Glu Arg Glu Lys Lys Glu Leu Ala Asp Ser Phe Ala Arg Val Ser
225                 230                 235                 240
Asp Gln Ala Gln Arg Lys Thr Gln Glu Gln Gln Asp Val Leu Glu Asn
                245                 250                 255
Leu Lys His Glu Leu Ala Thr Ser Arg Gln Glu Leu Gln Val Leu His
            260                 265                 270
Ser Asn Leu Glu Thr Ser Ala Gln Ser Glu Ala Lys Trp Leu Thr Gln
            275                 280                 285
Ile Ala Glu Leu Glu Lys Glu Gln Gly Ser Leu Ala Thr Val Ala Ala
            290                 295                 300
Gln Arg Glu Glu Glu Leu Ser Ala Leu Arg Asp Gln Leu Glu Ser Thr
305                 310                 315                 320
Gln Ile Lys Leu Ala Gly Ala Gln Glu Ser Met Cys Gln Gln Val Lys
            325                 330                 335
Asp Gln Arg Lys Thr Leu Leu Ala Gly Ile Arg Lys Ala Ala Glu Arg
            340                 345                 350
Glu Ile Gln Glu Ala Leu Ser Gln Leu Glu Glu Pro Thr Leu Ile Ser
            355                 360                 365
Cys Ala Gly Ser Thr Asp His Leu Leu Ser Lys Val Ser Ser Val Ser
            370                 375                 380
Ser Cys Leu Glu Gln Leu Glu Lys Asn Gly Ser Gln Tyr Leu Ala Cys
385                 390                 395                 400
Pro Glu Asp Ile Ser Glu Leu Leu His Ser Ile Thr Leu Leu Ala His
                405                 410                 415
Leu Thr Gly Asp Thr Val Ile Gln Gly Ser Ala Thr Ser Leu Arg Ala
            420                 425                 430
Pro Pro Glu Pro Ala Asp Ser Leu Thr Glu Ala Cys Arg Gln Tyr Gly
            435                 440                 445
Arg Glu Thr Leu Ala Tyr Leu Ser Ser Leu Glu Glu Glu Gly Thr Val
            450                 455                 460
Glu Asn Ala Asp Val Thr Ala Leu Arg Asn Cys Leu Ser Arg Val Lys
465                 470                 475                 480
Thr Leu Gly Glu Glu Leu Leu Pro Arg Gly Leu Asp Ile Lys Gln Glu
                485                 490                 495
Glu Leu Gly Asp Leu Val Asp Lys Glu Met Ala Ala Thr Ser Ala Ala
```

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```
                    500                      505                      510
    Ile Glu Ala Ala Thr Thr Arg Ile Glu Glu Ile Leu Ser Lys Ser Arg
            515                      520                      525
    Ala Gly Asp Thr Gly Val Lys Leu Glu Val Asn Glu Arg Ile Leu Gly
            530                      535                      540
    Ser Cys Thr Ser Leu Met Gln Ala Ile Lys Val Leu Val Val Ala Ser
    545                      550                      555                      560
    Lys Asp Leu Gln Lys Glu Ile Val Glu Ser Gly Arg Gly Ser Ala Ser
                    565                      570                      575
    Pro Lys Glu Phe Tyr Ala Lys Asn Ser Arg Trp Thr Glu Gly Leu Ile
                    580                      585                      590
    Ser Ala Ser Lys Ala Val Gly Trp Gly Ala Thr Ile Met Val Asp Ala
            595                      600                      605
    Ala Asp Leu Val Val Gln Gly Lys Gly Lys Phe Glu Glu Leu Met Val
            610                      615                      620
    Cys Ser Arg Glu Ile Ala Ala Ser Thr Ala Gln Leu Val Ala Ala Ser
    625                      630                      635                      640
    Lys Val Lys Ala Asn Lys Gly Ser Leu Asn Leu Thr Gln Leu Gln Gln
                    645                      650                      655
    Ala Ser Arg Gly Val Asn Gln Ala Thr Ala Ala Val Val Ala Ser Thr
                    660                      665                      670
    Ile Ser Gly Lys Ser Gln Ile Glu Glu Thr Asp Ser Met Asp Phe Ser
            675                      680                      685
    Ser Met Thr Leu Thr Gln Ile Lys Arg Gln Glu Met Asp Ser Gln Val
            690                      695                      700
    Arg Val Leu Glu Leu Glu Asn Asp Leu Gln Lys Glu Arg Gln Lys Leu
    705                      710                      715                      720
    Gly Glu Leu Arg Lys Lys His Tyr Glu Leu Glu Gly Val Ala Glu Gly
                    725                      730                      735
    Trp Glu Glu Gly Thr Glu Ala Ser Pro Ser Thr Val Gln Glu Ala Ile
                    740                      745                      750
    Pro Asp Lys Glu
            755
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<210> 10
<211> 3979
<212> DNA
<213> Mouse

<400> 10
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ggcgcgggtg ctgagccgca ggccgggcca cagcctagag gccgagcgcg agcagttcga    180
caagacgcag gccatcagta tcagcaaagc catcaacagc caggaggccc cagtgaagga    240
gaagcatgcc cggcgtatca tcctgggcac gcatcatgag aagggagcct tcaccttctg    300
gtcctatgcc atcggcctgc cgctgtccag cagctccatc ctcagctgga agttctgtca    360
cgtccttcac aaggtcctcc gggacggaca ccccaacgtc ctgcatgact atcagcggta    420
ccggagcaac atacgtgaga tcggtgactt gtggggccac cttcgtgacc agtatggaca    480
cctggtgaat atctatacca aactgttgct gactaagatc tccttccacc ttaagcaccc    540
ccagtttcct gcaggcctgg aggtaacaga tgaggtgttg gagaaggcgg cgggaactga    600
tgtcaacaac atttttcagc ttaccgtgga gatgtttgac tacatggact gtgaactgaa    660
gctttctgag tcagtttttc ggcagctcaa cacggccatc gcagtgtccc agatgtcttc    720
tggccagtgt cgcctagcgc cgctcatcca ggtcattcag gactgcagcc acctgtacca    780
ctacacagtg aagctcatgt ttaagctgca ctcctgtctc ccggcagaca ccctgcaagg    840
ccacagggat cggttccacg agcagttcca cagcctcaaa aacttcttcc gccgggcttc    900
agacatgctg tacttcaaga ggctcatcca gatcccgcgg ctgcctgagg acccccccaa    960
tttcctgcag gcttcagccc tggctgagca catcaagccg gtggtggtga ttcccgagga   1020
ggccccagag gaagaggagc ctgagaacct aattgaaatc agcagtgcgc cccctgctgg   1080
ggagccagtg gtggtggctg acctctttga tcagaccttt ggaccccca atggctccat   1140
gaaggatgac agggacctcc aaatcgagaa cttgaagaga gaggtggaga ccctccgtgc   1200
tgagctggag aagattaaga tggaggcaca gcggtacatc tcccagctga agggccaggt   1260
gaatggcctg gaggcagagc tggaggagca gcgcaagcag aagcagaagg ccctggtgga   1320
```

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Al

```
caacgagcag ctgcgccacg agctggccca gctcaaggcc ctgcagctgg agggcgcccg   1380
caaccagggc cttcgagagg aagcagagag gaaggccagt gccacggagg cacgctacag   1440
caagctgaag gagaaacaca gcgaactcat taacacgcac gccgagctgc tcaggaagaa   1500
cgcagacacg gccaagcagc tgacagtgac acagcgagagc caggaggagg tggcacgggt   1560
aaaggaacag ctggccttcc agatggagca agcgaagcgt gagtctgaga tgaagatgga   1620
agagcagagc gaccagttgg agaagctcaa gagggagctg gcggccaggg caggagagct   1680
ggcccgtgcg caggaggccc tgagccgcac agaacagagt gggtcagagc tgagctcacg   1740
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<210> 11
<211> 1068
<212> PRT
<213> Mouse

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<400> 11
Met Asn Ser Ile Lys Asn Val Pro Ala Arg Val Leu Ser Arg Arg Pro
1               5                   10                  15
Gly His Ser Leu Glu Ala Glu Arg Glu Gln Phe Asp Lys Thr Gln Ala
            20                  25                  30
Ile Ser Ile Ser Lys Ala Ile Asn Ser Gln Glu Ala Pro Val Lys Glu
        35                  40                  45
Lys His Ala Arg Arg Ile Ile Leu Gly Thr His His Glu Lys Gly Ala
    50                  55                  60
Phe Thr Phe Trp Ser Tyr Ala Ile Gly Leu Pro Leu Ser Ser Ser Ser
65                  70                  75                  80
```

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```
Ile Leu Ser Trp Lys Phe Cys His Val Leu His Lys Val Leu Arg Asp
                85                    90                    95
Gly His Pro Asn Val Leu His Asp Tyr Gln Arg Tyr Arg Ser Asn Ile
                100               105               110
Arg Glu Ile Gly Asp Leu Trp Gly His Leu Arg Asp Gln Tyr Gly His
            115               120               125
Leu Val Asn Ile Tyr Thr Lys Leu Leu Leu Thr Lys Ile Ser Phe His
        130               135               140
Leu Lys His Pro Gln Phe Pro Ala Gly Leu Glu Val Thr Asp Glu Val
145               150               155               160
Leu Glu Lys Ala Ala Gly Thr Asp Val Asn Asn Ile Phe Gln Leu Thr
                165               170               175
Val Glu Met Phe Asp Tyr Met Asp Cys Glu Leu Lys Leu Ser Glu Ser
            180               185               190
Val Phe Arg Gln Leu Asn Thr Ala Ile Ala Val Ser Gln Met Ser Ser
        195               200               205
Gly Gln Cys Arg Leu Ala Pro Leu Ile Gln Val Ile Gln Asp Cys Ser
    210               215               220
His Leu Tyr His Tyr Thr Val Lys Leu Met Phe Lys Leu His Ser Cys
225               230               235               240
Leu Pro Ala Asp Thr Leu Gln Gly His Arg Asp Arg Phe His Glu Gln
                245               250               255
Phe His Ser Leu Lys Asn Phe Phe Arg Arg Ala Ser Asp Met Leu Tyr
            260               265               270
Phe Lys Arg Leu Ile Gln Ile Pro Arg Leu Pro Glu Gly Pro Pro Asn
        275               280               285
Phe Leu Arg Ala Ser Ala Leu Ala Glu His Ile Lys Pro Val Val Val
    290               295               300
Ile Pro Glu Glu Ala Pro Glu Glu Glu Glu Pro Glu Asn Leu Ile Glu
305               310               315               320
Ile Ser Ser Ala Pro Pro Ala Gly Glu Pro Val Val Val Ala Asp Leu
            325               330               335
Phe Asp Gln Thr Phe Gly Pro Pro Asn Gly Ser Met Lys Asp Asp Arg
        340               345               350
Asp Leu Gln Ile Glu Asn Leu Lys Arg Glu Val Glu Thr Leu Arg Ala
    355               360               365
Glu Leu Glu Lys Ile Lys Met Glu Ala Gln Arg Tyr Ile Ser Gln Leu
    370               375               380
Lys Gly Gln Val Asn Gly Leu Glu Ala Glu Leu Glu Glu Gln Arg Lys
385               390               395               400
Gln Lys Gln Lys Ala Leu Val Asp Asn Glu Gln Leu Arg His Glu Leu
            405               410               415
Ala Gln Leu Lys Ala Leu Gln Leu Glu Gly Ala Arg Asn Gln Gly Leu
        420               425               430
Arg Glu Glu Ala Glu Arg Lys Ala Ser Ala Thr Glu Ala Arg Tyr Ser
    435               440               445
Lys Leu Lys Glu Lys His Ser Glu Leu Ile Asn Thr His Ala Glu Leu
    450               455               460
Leu Arg Lys Asn Ala Asp Thr Ala Lys Gln Leu Thr Val Thr Gln Gln
465               470               475               480
Ser Gln Glu Glu Val Ala Arg Val Lys Glu Gln Leu Ala Phe Gln Met
            485               490               495
Glu Gln Ala Lys Arg Glu Ser Glu Met Lys Met Glu Glu Gln Ser Asp
        500               505               510
Gln Leu Glu Lys Leu Lys Arg Glu Leu Ala Ala Arg Ala Gly Glu Leu
    515               520               525
Ala Arg Ala Gln Glu Ala Leu Ser Arg Thr Glu Gln Ser Gly Ser Glu
    530               535               540
Leu Ser Ser Arg Leu Asp Thr Leu Asn Ala Glu Lys Glu Ala Leu Ser
545               550               555               560
Gly Val Val Arg Gln Arg Glu Ala Glu Leu Leu Ala Ala Gln Ser Leu
            565               570               575
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```
Val Arg Glu Lys Glu Glu Ala Leu Ser Gln Glu Gln Gln Arg Ser Ser
        580                 585                 590
Gln Glu Lys Gly Glu Leu Arg Gly Gln Leu Ala Glu Lys Glu Ser Gln
        595                 600                 605
Glu Gln Gly Leu Arg Gln Lys Leu Leu Asp Glu Gln Leu Ala Val Leu
    610                 615                 620
Arg Ser Ala Ala Ala Glu Ala Glu Ala Ile Leu Gln Asp Ala Val Ser
625                 630                 635                 640
Lys Leu Asp Asp Pro Leu His Leu Arg Cys Thr Ser Ser Pro Asp Tyr
                645                 650                 655
Leu Val Ser Arg Ala Gln Ala Ala Leu Asp Ser Val Ser Gly Leu Glu
            660                 665                 670
Gln Gly His Thr Gln Tyr Leu Ala Ser Ser Glu Asp Ala Ser Ala Leu
        675                 680                 685
Val Ala Ala Leu Thr Arg Phe Ser His Leu Ala Ala Asp Thr Ile Val
        690                 695                 700
Asn Gly Ala Ala Thr Ser His Leu Ala Pro Thr Asp Pro Ala Asp Arg
705                 710                 715                 720
Leu Met Asp Thr Cys Arg Glu Cys Gly Ala Arg Ala Leu Glu Leu Val
                725                 730                 735
Gly Gln Leu Gln Asp Gln Thr Val Leu Arg Arg Ala Gln Pro Ser Leu
            740                 745                 750
Met Arg Ala Pro Leu Gln Gly Ile Leu Gln Leu Gly Gln Asp Leu Lys
        755                 760                 765
Pro Lys Ser Leu Asp Val Arg Gln Glu Glu Leu Gly Ala Met Val Asp
    770                 775                 780
Lys Glu Met Ala Ala Thr Ser Ala Ala Ile Glu Asp Ala Val Arg Arg
785                 790                 795                 800
Ile Glu Asp Met Met Ser Gln Ala Arg His Glu Ser Ser Gly Val Lys
                805                 810                 815
Leu Glu Val Asn Glu Arg Ile Leu Asn Ser Cys Thr Asp Leu Met Lys
            820                 825                 830
Ala Ile Arg Leu Leu Val Met Thr Ser Thr Ser Leu Gln Lys Glu Ile
        835                 840                 845
Val Glu Ser Gly Arg Gly Ala Ala Thr Gln Gln Glu Phe Tyr Ala Lys
    850                 855                 860
Asn Ser Arg Trp Thr Glu Gly Leu Ile Ser Ala Ser Lys Ala Val Gly
865                 870                 875                 880
Trp Gly Ala Thr Gln Leu Val Glu Ser Ala Asp Lys Val Val Leu His
                885                 890                 895
Met Gly Lys Tyr Glu Glu Leu Ile Val Cys Ser His Glu Ile Ala Ala
            900                 905                 910
Ser Thr Ala Gln Leu Val Ala Ala Ser Lys Val Lys Ala Asn Lys Asn
        915                 920                 925
Ser Pro His Leu Ser Arg Leu Gln Glu Cys Ser Arg Thr Val Asn Glu
    930                 935                 940
Arg Ala Ala Asn Val Val Ala Ser Thr Lys Ser Gly Gln Glu Gln Ile
945                 950                 955                 960
Glu Asp Arg Asp Thr Met Asp Phe Ser Gly Leu Ser Leu Ile Lys Leu
                965                 970                 975
Lys Lys Gln Glu Met Glu Thr Gln Val Arg Val Leu Glu Leu Glu Lys
            980                 985                 990
Thr Leu Glu Ala Glu Arg Val Arg Leu Gly Glu Leu Arg Lys Gln His
        995                 1000                1005
Tyr Val Leu Ala Gly Gly Met Gly Thr Pro Ser Glu Glu Glu Pro Ser
    1010                1015                1020
Arg Pro Ser Pro Ala Pro Arg Ser Gly Ala Thr Lys Lys Pro Pro Leu
1025                1030                1035                1040
Ala Gln Lys Pro Ser Ile Ala Pro Arg Thr Asp Asn Gln Leu Asp Lys
                1045                1050                1055
Lys Asp Gly Val Tyr Pro Ala Gln Leu Val Asn Tyr
            1060                1065
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<210> 12
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> sequencing primer

<400> 12
gaagataccc caccaaac                                                      18

<210> 13
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> cDNA primer

<400> 13
gcttgacagt gtagtcataa aggtggctgc agtcc                                   35

<210> 14
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 14
ggacatgtcc agggagttga atac                                               24

<210> 15
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 15
cuacuacuac uacuaggcca cgcgtcgact agtacggggg ggggg                        45

<210> 16
<211> 516
<212> DNA
<213> Human

<400> 16
tctgtggaag gtttggaggg gagagagggg cagctggatg ctcttgggcc acggtcgccc        60
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gcatctcttt gtgcgggctt taattgccat gttgttgtgc caagggagtg agtggcggcg       180
ggaccagcag ctgggcacag ccaatgccag gcagtggtgc ccactccctc aggacgccca       240
gccagctggc tcctgggagc gctgcccacc tctgccccca gctgggcgcc tgcaaggaac       300
cgaccacccg tggggctggg ggaggttggc tggaggagga gaaaggggcg ggctctggga       360
gggtctcagc cactctcaga ggcttattca tctcatcctc ctttccctcc cccttcttgt       420
ttttcagact gtcagcatca ataaggccat taatacgcag gaagtggctg taaaggaaaa       480
acacgccaga aatatccttt ggatgttgct tggaag                                 516

<210> 17
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<211> 193
<212> DNA
<213> Human

<400> 17
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gaccttctgg tctgttgtca accgcctgcc tctgtctagc aacccagtgc tctgctggaa   120
gttctgccat gtgttccaca aactcctccg agatggacac ccgaacgtga gttcctgggg   180
ctatggggtg gca   193

<210> 18
<211> 104
<212> DNA
<213> Human

<400> 18
gtgttctttt gcccctgcag gtcctgaagg actctctgag atacagaaat gaattgagtg   60
acatgagcag gatgtgggtg agtttggaga tgtactcagg agcc   104

<210> 19
<211> 327
<212> DNA
<213> Human

<400> 19
aattcctggc tgcagatctc ttgactgtta tgttcttgtt gttgactctg tttcccctcc   60
tcttcctaaa agggccacct gagcgagggg tatggccagc tgtgcagcat ctacctgaaa   120
ctgctaagaa ccaagatgga gtaccacacc aaagtgagtc tctgcggaca gttctgccgc   180
caccgccgcc tcccctgctc catcccttca gcccctccct gggctcattt gtcagctctt   240
tcaggtaata gacagcccag gcttctgagg aagtgtgcac atcatgtacc caagctgtga   300
gagaggaaag ccaccgccag gcccacg   327

<210> 20
<211> 331
<212> DNA
<213> Human

<400> 20
gggctcaagc aatcctccca cctcggcctc ccaagtagct gggaccacag gcgtgtgcca   60
ccacgcccgg ctgagagagg gctcttcatg tcttctgcct tgactccctt cctctgcctc   120
ccttccagaa tcccaggttc ccaggcaacc tgcagatgag tgaccgccag ctggacgagg   180
ctggagaaag tgacgtgaac aacttgtaag tggctcctgc cctgagccca gggagggaga   240
aagcttttgt gaatgctgac acttctcata agggtcatgg agggcctgat gggggggaggc   300
cgtggctggg atggggacca aagcccctgg g   331

<210> 21
<211> 470
<212> DNA
<213> Human

<400> 21
actgtcgctg tcactgttga cttcaccagg ctgcatggcc ataatacccca caaggctaag   60
acttggagct ggagttgtgt gtgtgtttgc gcatgcacat gagcattgga gactggagta   120
gcgtagagcg tggggggaggg gacaggtaac agaccggcct caggctgtgg agtgtaagct   180
ctctttcctc ttgggtccag tttccagtta acagtggaga tgtttgacta cctggagtgt   240
gaactcaacc tcttccaaac aggtgagtct cttccctccc gtctaaccca ggctctcatg   300
ggaactacct aattcctagt cctcctctcc ctgcaaagtg tgcagcacaa ggggtaggaa   360
aatggagaca ttcacacccc atctctggtc tctccaaccc tcgtgcaggg agggactgaa   420
cctcttcagt attttttcttt ttaagagaca aggtctcggc cgggtgcagt   470

<210> 22
<211> 565

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```
<212> DNA
<213> Human

<400> 22
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tctgcccctc tgaagaggct gcctgtaatc ccctggctct accaccttttc tccctcactt     180
ttatttccta gtattcaact ccctggacat gtcccgctct gtgtccgtga cggcagcagg     240
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cactgtcaag cttctcttca aactccactc ctgtgagtac cgcgggccag atcttcttac     360
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ttctcagtgc ctttggctgt ctgcttctgt tccaaaaggc cccggagctt ctgaccattg     480
tgaggataaa agagcagggc ccaggctttg gtgaccccag taaagcccct ggcttgccac     540
tcttgcgtcc agtgttacag gatct                                          565

<210> 23
<211> 233
<212> DNA
<213> Human

<400> 23
gggacagctc taggccagtc gtggcccctg gcagtgctgg ccacatgccc cagggtagct      60
gggcccctcc ccctcgagag ccccgctgtg gcttccctgc cctctggtcc ccctcccctc     120
tcacactctt tccaatttct tccaggcctc ccagctgaca ccctgcaagg ccaccgggac     180
cgcttcatgg agcagtttac aaagtaagtg gttcaagtaa caggaatgga ggt           233

<210> 24
<211> 578
<212> DNA
<213> Human

<400> 24
tgaatcccag caccatggag tttatctcct tgacagcctg tgcctttggg ctggggaggg      60
ggcaggaaag ccaggtggct gctctgtccc ctacatgggg ctgatgaaga cacccagcac     120
ccctcaggtc cttctccacc cctaggttga aagatctgtt ctaccgctcc agcaacctgc     180
agtacttcaa gcggctcatt cagatccccc agctgcctga ggtaagcatg cccaaccaca     240
caccctcggc actgcagagg ccccaggtac tctcttaagg gccggcgggg cctggcaagc     300
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gccctgtcag aacatatcag ccctgtggtg gtgatccctg cagaggcctc atcccccgac     420
agcgagccag tcctagagaa ggatgacctc atggacatgg atgcctctca gcaggtgagg     480
accacttggg agagaaactt ggcctttcct ctcacctgca agtacagggg agaggctggg     540
ggagaccctg gccaaagccc attgactcta accaggtt                            578

<210> 25
<211> 390
<212> DNA
<213> Human

<400> 25
aaaaaaattt aaaaaattaa acaggtctga accgtttaat tcgagaaagg gggcattctc      60
ccatatcact caactgaccc acacacagaa ttctctggct ctctgactta ttctcactcc     120
tttttggtca accacagaat ttatttgaca acaagtttga tgacatcttt ggcagttcat     180
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cactaaccaa agaggaattc ttaatgatac tggggcttct tagatacaga acatcttgaa     360
gggttggggg caatggctta tgcctgtaat                                     390

<210> 26
<211> 547
<212> DNA
<213> Human
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```
<400> 26
aaaatcaata accatggatt tatgagtatt agattagtat ctggtaacat ttagagtata      60
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agctcacaat taaaaacaga gggatagaag cactatgaaa gcaaactcat tcccttctc      180
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cacggtagat ttgaatgtta aatttgcatc acactagcca ggcacagtgg ctcacacctg     360
taatcctagc actttgggag gccaaggcag gaggattacc tgaggtcggg agttcgagac     420
cagcctgggc aacagggtga aaccccgtc ttcaataaaa atgcaataat tagccgggtg      480
tgttggcagg cacctgtaat cccagctact cgggaagctg aggcatgaga attgcttgaa     540
cttggga                                                              547

<210> 27
<211> 436
<212> DNA
<213> Human

<400> 27
ccccagcca ctctaaagag gaccacaatt ccccggccat catcccctgt tattgttgtt       60
gattgagggg ctcctaatga ccagatggtc caaccctcct gggacgtgga gagttgactt     120
aggggaatca ggtatttact tggaagcatg gtaggacccg cttctccggc ccatgcccgt     180
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ctgcggcagc aggcggccga cgactgtgaa ttcctgcggg cagaactgga cgagctcagg     360
aggcagcggg aggacaccga gaaggctcag cggagcctgt ctgagataga aagtgagcgg     420
tgggtggggg cggggg                                                    436

<210> 28
<211> 469
<212> DNA
<213> Human

<400> 28
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ctcattgcaa ggaaggcaag ggtccctgct aggttagact cctcaccttg gtcctttaca     180
atacagggaa agctcaagcc aatgaacagc gatatagcaa gctaaaggag aagtacagcg     240
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agcaaccct acattgatct ctaaggcatt gccgtcatct cgggaaccac accttttcag      420
gcttccttgc ctctgtgtct tgggctgtgt cctgggtgcc aatcccatg                469

<210> 29
<211> 359
<212> DNA
<213> Human

<400> 29
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ctagaaggag gatgtcctct aagcctggga tctcctggtt caagacactg ttcttctttt     120
gcagaatgca gaggtgacca aacaggtgtc catggccaga caagcccagg tagatttgga     180
acgagagaaa aaagagctgg aggattcgtt ggagcgcatc agtgaccagg gccagcggaa     240
ggtgagtggg acgaggagca ctcgggaaat gagggagggg gctgttgagt tggtggcggg     300
ggctttgtgg ccttctgctc catgggcagt tctgtgggtc ggttggcatc acacagcag     359

<210> 30
<211> 209
<212> DNA
<213> Human

<400> 30
gttgatcgct tgggacgttt ttacattttt atattctttg tcactgtcac ccagatcaga       60
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gtccctctgt ttttcttctc tttcagactc aagaacagct ggaagttcta gagagcttga    120
agcaggaact tgccacaagc caacgggagc ttcaggttct gcaaggcagc ctggaaactt    180
ctgcccaggt aaatacctcc ttttttttt                                      209
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<210> 31
<211> 485
<212> DNA
<213> Human

<400> 31
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cccccactgc aatcagtgtg tccccgggag ggaatcagag tggcaggtta aagagccatc     60
accttcccag tccttgcaac ccggtggtgg gttggacctc tgggaagtag ggactgttta    120
actcaaccag cgtctccctc tttccttgtg gtcacctttg cagtcagaag caaactgggc    180
agccgagttc gccgagctag agaaggagcg ggacagcctg gtgagtggcg cagctcatag    240
ggaggaggaa ttatctgctc ttcggaaaga actgcaggac actcagctca aactggccag    300
cacagagggt cacggacatg gacacgagcg agcacctgtg aattcccacc gagggcctct    360
gcgcatgcac ggaggctggg aggaccccgg ggctgctgag aaggggtttg gggccttggc    420
ctgattgtgc agacattctg taggtgtaat gccagcaggc cctgcattgc ctgcagagtc    480
catga                                                                485
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<210> 32
<211> 468
<212> DNA
<213> Human

<400> 32
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gctgcgctgg gtctgccaggt acacttgcaa ttgccagct ggcaggggcc aggtccttac    300
agcctgagac tctgttgatg ttgaatctca tgtgagactt agctcagggg ctctcagccc    360
agcagcatgt cagcattacc ttaggggcgc ccaggcccca tcctagatca gttacatgtg    420
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<210> 33
<211> 393
<212> DNA
<213> Human

<400> 33
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tttccagctg catcgagcaa ctggagaaaa gctggagcca gtatctggcc tgcccagaag    180
gtaagaatgg ccaaggacag tctctgtcgg ctagtgatgg ccagacaggg ttcagaagca    240
cctgaatgcg gggatagtga caggtccctc tgcatcaaga aaggcatgta ggcaactcat    300
acaagaaagg catgtaggca actcataaaa cgggaggaga gggtatgaaa gtgtcaccat    360
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<210> 34
<211> 421
<212> DNA
<213> Human

<400> 34
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tgtaggcaac tcatacaaga aaggcatgta ggcaactcat aaaacgggag gagagggtat    180
gaaagtgtca ccatcaacca gacctgagaa acttctcttt ccaatcctgg cagacatcag    240
tggacttctc cattccataa ccctgctggc ccacttgacc agcgacgcca ttgctcatgg    300
tgccaccacc tgcctcagag ccccacctga gcctgccgac tgtgagtact ggggcatgag    360
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<211> 498
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attgccttgt atctccagca ctgaccgagg cctgtaagca gtatggcagg gaaaccctcg     180
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<210> 36
<211> 427
<212> DNA
<213> Human

<400> 36
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ttcacaggag ctcctgccca ggggactgga catcaagcag gaggagctgg gggacctggt     180
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gaatttgcca ggcacagtgg ctcatgcctg taaccccagc accttgggag gatcacttga     420
gtccagg                                                             427

<210> 37
<211> 367
<212> DNA
<213> Human

<400> 37
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taagacatta gtggatcctt aatattcaag gcacatttag aaaccatgct tctttttcac     180
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tgagttg                                                             367

<210> 38
<211> 502
<212> DNA
<213> Human

<400> 38
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cagtgtatcc tcgacttgtt tgtttggcag gatccttggt tgctgtacca gcctcatgca     180
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cagggtgagc gtgggtgtgg gccctgggca ggaagaggag gcatcggtga cagactcccg     300
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<210> 39
<211> 437
<212> DNA
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<400> 39
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gctcaataaa aggtggctat tactatttt tatttcccta gggtacagca tcccctaaag      180
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aaataaaacta ttgatcagga agtcaatagg accgagttta caagggagcc tggctctccc     420
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<210> 40
<211> 351
<212> DNA
<213> Human

<400> 40
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<210> 41
<211> 418
<212> DNA
<213> Human

<400> 41
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<210> 42
<211> 279
<212> DNA
<213> Human

<400> 42
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<210> 43
<211> 3715
<212> DNA
<213> Human

<400> 43
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